

FASTA searches a protein or DNA sequence data bank
version 3.3t05 March 30, 2000

Please cite:

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

```
/tmp/fastaCAAygaWej: 995 aa
>SEQ ID NO:2
vs /tmp/fastaDAAzgaWej library
searching /tmp/fastaDAAzgaWej library
```

1008 residues in 1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2
join: 39, opt: 27, gap-pen: -12/ -2, width: 16

Scan time: 0.034

The best scores are:
M13699 ACCESSION:M13699 NID: gi 180255 gb M13699. (1008) 2671

opt

```
>>M13699 ACCESSION:M13699 NID: gi 180255 gb M13699.1 HUM (1008 aa)
initn: 1414 initl: 972 opt: 2671
Smith-Waterman score: 3980; 57.002% identity in 1014 aa overlap (1-992:1-1008)
```

	10	20	30	40	50
SEQ	MKILILGIFLFLCSSPGWAIDRHCYIGIEESIWNYAPSGKNMLNEKPFSEDLE---FLQ				

M13699	MKILILGIFLFLCSTPAWAKEKHYYIGIIETTWDYA---SDHGEKKLISVDTEHSNIYLQ				
	10	20	30	40	50

	60	70	80	90	100	110
SEQ	GGQARKSFVFKKALYFQYTDNTFQRIIEKPWSLGFLGPMIKAETGDFIYVHVKNMASRAY					

M13699	NGPDRIGRLYKKALYQYTDETFRRTIEKPVWLGFGLGPIIKAETGDKVYVHLKNLASRPY					
	60	70	80	90	100	110

	120	130	140	150	160	170
SEQ	SYPHGLTYSKENEAHGAIYPDNTTGLQKEVEYLEPGKQYTYKWKYVEEHQGPGPNDSCV					

M13699	TFHSHGITYYYKEHE--GAIYPDNTTDFQRADDKVYPGEQYTYMLLATEEQSPGEGDGNCV					
	120	130	140	150	160	170

	180	190	200	210	220	230
SEQ	TRIYHSHIDTARDVASGLIGPLTCKRGTLNGDTEKDIDRSSFLMFSTTDESRSWYSDEN					

M13699	TRIYHSHIDAPKDIASGLIGPLIICKKDSLDEKEKEKHIDREFVVMFSVVDENFSWYLEDN					
	180	190	200	210	220	230

	240	250	260	270	280	290
SEQ	IRAF-TESGKINTSDPRFEESMSMQSINGYIYGNLPNLTMCAEDRVQWYFVGGMGVADIH					

M13699	IKTYCSEPEKVDKDNEFQESNRMYSVNGYTFGSLPGLSMCAEDRVKWYLFGMGNEDVH					
	240	250	260	270	280	290

	300	310	320	330	340	350
SEQ	PVYLRGQTLISRNRKDTIMLFPSLEDAFMVAKAPGVWMLGCQ---IHESMQAFFKVS					

M13699	AAFFHGQALTNKNYRIDTINLFPATLFDAYMVAQNPGEWMLSCQNLNHLKAGLQAFFQVQ					
	300	310	320	330	340	350

	360	370	380	390	400	410
SEQ	NCQKPSTEAFVTGTHVIHYYIAAKEILWNYAPSGIDFFTKKNLTAAGSKSQLFFERSPTR					
M13699	ECNKSSSKDNIRGKHVRHYYIAAEEIIWNYAPSGIDIFTKENLTAPGSDSAVFFEQQGTR	360	370	380	390	400
						410
	420	430	440	450	460	470
SEQ	IGGYKKLIVREYTDASFQTQKAR---EEHLGILGPVFKAEVGQTIKITFYNNASLPLSI					
M13699	IGGSYKKLVYREYTDASFNRKERGPEEEHLGILGPVIWAEVGDTIRVTFHNGAYPLSI	420	430	440	450	460
						470
	480	490	500	510	520	530
SEQ	QPPGLHYNKSNEGLFYE---TPGG-STPPPSSHVSPGTTFVYTWEVPKDVGPTSTDPNCL					
M13699	EPIGVRFNKNNEGTYYSPPNQSPRSVPPSASHVAPTEFTYEWTVPKEVGPTNADPVCL	480	490	500	510	520
						530
	540	550	560	570	580	590
SEQ	TWFYYSSVNGKKDINSGLGPLLICRNGSLGDDGKQKGVDKEFYLLATIFDENESNLLDE					
M13699	AKMYYSAVDPTKDIIFTGLIGPMKICKKGSLLHANGRQKDVKEFYLFPFTVDENESLLLED	540	550	560	570	580
						590
	600	610	620	630	640	650
SEQ	N-RTFITEPENIDKEDTDCQASNKMYISINGYMYGNLPGLDTCLGDNVLWHVFSVGSVEDL					
M13699	NIRMFTTAPDQVDKEDEDFAQESNKMHSMNGFMYGNQPLTMCKGDSVVWYLFSAQNEADV	600	610	620	630	640
						650
	660	670	680	690	700	710
SEQ	HGIYFSGNTFTSLGARRDTIPMFPTYSQTLMTPSIGTFDLVCMTIKHNLGGMKHKYHV					
M13699	HGIYFSGNTYLWRGERRDATANLFPQTSLTLHMWPDTETGFNFVECLTDHYTGGMQKYTV	660	670	680	690	700
						710
	720	730	740	750	760	770
SEQ	RQCQKPNPDQTQYQEEKIIITIAAEEMEWDYSPSRKWENELHHLRRENQTSMYVDRSGTL					
M13699	NQCRRQSEDSTFYLGERTYY-IAAVEVEWDYSPQREWEKELHHLQEQNVSNAFLDKGEFY	720	730	740	750	760
						770
	780	790	800	810	820	830
SEQ	LGSKYKKVLYRQYDDNTFTNQTKRNEGEKHLDILGPLILLNPQIIQIIFKNKAARPYSI					
M13699	IGSKYKKVYRQYTDSTFRVPVERKAEEEHLGILGPQLHADVGDKVKIIIFKNMATRPYI	780	790	800	810	820
						830
	840	850	860	870	880	890
SEQ	HAHGVTNNSTVVPTQPGEIQIYTWQIPDRTGPTSLDFECIPWFYYSTVSVAKDLHSGLV					
M13699	HAHGVTESSTVTPLPGETLTYWKIPERSGAGTEDSACIPWAYYSTVDQVKDLYSGLI	840	850	860	870	880
						890

	890	900	910	920	930		
SEQ	GPLSVCR	---KDINPN	-IVHRVLHFMIFDENESWYFEDSINTYASKPNKVDKENDNFQL				
	::: :::	::: ..	::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::				
M13699	GPLIVCRRPYLKVFNP	RRKLEFALLFLV	DENESWYLD	NIKYSDHPEKVN	KDDEEFIE		
	900	910	920	930	940	950	
	940	950	960	970	980	990	
SEQ	SNQMHAINGRLFGNNQ	GITFHVG	DEVNNWY	LIGIGNEADL	HTVHF	GHSFEYKH	KYLI
	::: :::::	::: :::::	::: :::::	::: :::::	::: :::::	::: :::::	::: :::::
M13699	SNKMHAINGRMFGNLQ	GLTMHG	DEVNWYLM	MGMGNEIDL	HTVHF	GHSF	QYKHR
	960	970	980	990	1000		

995 residues in 1 query sequences

1008 residues in 1 library sequences

Scomplib [version 3.3t05 March 30, 2000]

start: Wed Sep 18 11:18:07 2002 done: Wed Sep 18 11:18:08 2002

Scan time: 0.034 Display time: 1.433

Function used was FASTA